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RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/09/924,099

TIME: 18:44:07

Input Set : N:\Crf3\RULE60\09924099.raw

Output Set: N:\CRF3\01142002\I924099.raw

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1 <110> APPLICANT: NISHIDA, Yoshihiro
2      OKURA, Takanori
3      TANIMOTO, Tadao
4      KURIMOTO, Masashi
5 <120> TITLE OF INVENTION: PEPTIDE
6 <130> FILE REFERENCE:
7 <140> CURRENT APPLICATION NUMBER: US/09/924,099
8 <141> CURRENT FILING DATE: 2001-08-08
9 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
W--> 10 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
11 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
W--> 12 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
13 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
W--> 14 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
15 <160> NUMBER OF SEQ ID NOS: 33
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18 <211> LENGTH: 108
19 <212> TYPE: PRT
20 <213> ORGANISM: Mus musculus
21 <400> SEQUENCE: 1
22      Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
23      1              5              10              15
24      Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly Ser Lys
25      20              25              30
26      Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg Leu Ile
27      35              40              45
28      Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
29      50              55              60
30      Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
31      65              70              75              80
32      Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser Pro Tyr
33      85              90              95
34      Thr Phe Gly Gly Gly Thr Lys Leu Ala Ile Lys Arg
35      100             105
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 113
39 <212> TYPE: PRT
40 <213> ORGANISM: Mus musculus
41 <400> SEQUENCE: 2
42      Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
43      1              5              10              15
44      Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
45      20              25              30
46      Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
47      35              40              45
48      Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
49      50              55              60

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50      Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe
51      65                      70                      75                      80
52      Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
53                      85                      90                      95
54      Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser
55                      100                      105                      110
56      Ala
58 <210> SEQ ID NO: 3
59 <211> LENGTH: 11
60 <212> TYPE: PRT
61 <213> ORGANISM: Mus musculus
62 <400> SEQUENCE: 3
63      Arg Ala Ser Gln Asp Ile Gly Ser Lys Leu Tyr
64      1                      5                      10
66 <210> SEQ ID NO: 4
67 <211> LENGTH: 7
68 <212> TYPE: PRT
69 <213> ORGANISM: Mus musculus
70 <400> SEQUENCE: 4
71      Ala Thr Ser Ser Leu Asp Ser
72      1                      5
74 <210> SEQ ID NO: 5
75 <211> LENGTH: 9
76 <212> TYPE: PRT
77 <213> ORGANISM: Mus musculus
78 <400> SEQUENCE: 5
79      Leu Gln Tyr Ala Ser Ser Pro Tyr Thr
80      1                      5
82 <210> SEQ ID NO: 6
83 <211> LENGTH: 10
84 <212> TYPE: PRT
85 <213> ORGANISM: Mus musculus
86 <400> SEQUENCE: 6
87      Gly Tyr Ser Phe Thr Asp Tyr Phe Ile Tyr
88      1                      5                      10
90 <210> SEQ ID NO: 7
91 <211> LENGTH: 17
92 <212> TYPE: PRT
93 <213> ORGANISM: Mus musculus
94 <400> SEQUENCE: 7
95      Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Arg
96      1                      5                      10                      15
97      Asp
99 <210> SEQ ID NO: 8
100 <211> LENGTH: 4
101 <212> TYPE: PRT
102 <213> ORGANISM: Mus musculus
103 <400> SEQUENCE: 8
104      Gly Leu Arg Phe

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105      1
107 <210> SEQ ID NO: 9
108 <211> LENGTH: 237
109 <212> TYPE: PRT
110 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Artificially produced peptide in the form of a single
113      chain
114      variable region fragment (scFv) which neutralizes IL-18
115 <400> SEQUENCE: 9
116      Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
117      1          5          10          15
118      Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
119      20          25          30
120      Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
121      35          40          45
122      Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
123      50          55          60
124      Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe
125      65          70          75          80
126      Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
127      85          90          95
128      Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser
129      100         105         110
130      Ala Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
131      115         120         125
132      Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
133      130         135         140
134      Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly
135      145         150         155         160
136      Ser Lys Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg
137      165         170         175
138      Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe
139      180         185         190
140      Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu
141      195         200         205
142      Glu Ser Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser
143      210         215         220
144      Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Ala Ile Lys
145      225         230         235
147 <210> SEQ ID NO: 10
148 <211> LENGTH: 243
149 <212> TYPE: PRT
150 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Artificially produced peptide in the form of a single
153      chain
154      variable region fragment (scFv) which neutralizes IL-18
155 <400> SEQUENCE: 10

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156	Glu	Ile	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Ala	
157	1				5					10					15		
158	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Thr	Asp	Tyr	
159				20					25					30			
160	Phe	Ile	Tyr	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Ser	Leu	Glu	Trp	Ile	
161			35					40					45				
162	Gly	Asp	Ile	Asp	Pro	Tyr	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe	
163		50					55					60					
164	Arg	Asp	Lys	Ala	Thr	Leu	Thr	Val	Asp	Gln	Ser	Ser	Thr	Thr	Ala	Phe	
165	65					70					75					80	
166	Met	His	Leu	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys	
167				85					90					95			
168	Ala	Arg	Gly	Leu	Arg	Phe	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	
169				100					105					110			
170	Ala	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
171			115					120					125				
172	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	
173		130					135					140					
174	Leu	Gly	Glu	Arg	Val	Ser	Leu	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Gly	
175	145					150				155						160	
176	Ser	Lys	Leu	Tyr	Trp	Leu	Gln	Gln	Glu	Pro	Asp	Gly	Thr	Phe	Lys	Arg	
177				165					170					175			
178	Leu	Ile	Tyr	Ala	Thr	Ser	Ser	Leu	Asp	Ser	Gly	Val	Pro	Lys	Arg	Phe	
179			180						185					190			
180	Ser	Gly	Ser	Arg	Ser	Gly	Ser	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Leu	
181		195						200					205				
182	Glu	Ser	Glu	Asp	Phe	Val	Asp	Tyr	Tyr	Cys	Leu	Gln	Tyr	Ala	Ser	Ser	
183		210					215					220					
184	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Ala	Ile	Lys	His	His	His	
185	225				230					235						240	
186	His	His	His														
188	<210>	SEQ ID NO:	11														
189	<211>	LENGTH:	324														
190	<212>	TYPE:	DNA														
191	<213>	ORGANISM:	Mus musculus														
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193	gac	atc	cag	atg	acc	cag	tct	cca	tcc	tcc	tta	tct	gcc	tct	ctg	gga	48
194	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly	
195	1				5					10					15		
196	gaa	aga	gtc	agt	ctc	act	tgt	cgg	gca	agt	cag	gac	att	ggt	agt	aaa	96
197	Glu	Arg	Val	Ser	Leu	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Gly	Ser	Lys	
198			20						25				30				
199	tta	tac	tgg	ctt	caa	cag	gaa	cca	gat	gga	act	ttt	aaa	cgc	ctg	atc	144
200	Leu	Tyr	Trp	Leu	Gln	Gln	Glu	Pro	Asp	Gly	Thr	Phe	Lys	Arg	Leu	Ile	
201		35					40					45					
202	tac	gcc	aca	tcc	agt	tta	gat	tct	ggt	gtc	ccc	aag	agg	ttc	agt	ggc	192
203	Tyr	Ala	Thr	Ser	Ser	Leu	Asp	Ser	Gly	Val	Pro	Lys	Arg	Phe	Ser	Gly	
204		50					55					60					
205	agt	agg	tct	ggg	tca	gat	tat	tct	ctc	acc	atc	agc	agc	ctt	gag	tct	240

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206      Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
207          65                      70                      75                      80
208      gaa gat ttt gta gac tat tac tgt cta caa tat gct agt tct ccg tac 288
209      Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser Pro Tyr
210                      85                      90                      95
211      acg ttc gga ggg ggg acc aag ctg gca ata aaa cgg 324
212      Thr Phe Gly Gly Gly Thr Lys Leu Ala Ile Lys Arg
213                      100                      105
215 <210> SEQ ID NO: 12
216 <211> LENGTH: 339
217 <212> TYPE: DNA
218 <213> ORGANISM: Mus musculus
219 <400> SEQUENCE: 12
220      gag atc cag ctg cag cag tct gga cct gag ctg gtg aag cct ggg gct 48
221      Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
222          1                      5                      10                      15
223      tca gtg aag gtc tcc tgt aag gct tct ggt tac tca ttc act gac tac 96
224      Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
225                      20                      25                      30
226      ttc att tac tgg gtg aag cag agc cat gga aag agc ctt gag tgg att 144
227      Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
228                      35                      40                      45
229      gga gat att gat cct tat aat ggt gat act agt tac aac cag aag ttc 192
230      Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
231          50                      55                      60
232      agg gac aag gcc aca ttg act gtt gac cag tcc tcc acc aca gcc ttc 240
233      Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe
234          65                      70                      75                      80
235      atg cat ctc aac agc ctg aca tct gag gac tct gca gtc tat ttc tgt 288
236      Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
237                      85                      90                      95
238      gca aga ggc cta cgg ttc tgg ggc caa ggg act ctg gtc act gtc tct 336
239      Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser
240                      100                      105                      110
241      gca 339
242      Ala
244 <210> SEQ ID NO: 13
245 <211> LENGTH: 33
246 <212> TYPE: DNA
247 <213> ORGANISM: Mus musculus
248 <400> SEQUENCE: 13
249      cgg gca agt cag gac att ggt agt aaa tta tac 33
250      Arg Ala Ser Gln Asp Ile Gly Ser Lys Leu Tyr
251          1                      5                      10
253 <210> SEQ ID NO: 14
254 <211> LENGTH: 21
255 <212> TYPE: DNA
256 <213> ORGANISM: Mus musculus
257 <400> SEQUENCE: 14

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/924,099

DATE: 01/14/2002

TIME: 18:44:08

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L:12 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:408 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:429 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:524 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:563 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28